OM protein - protein search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: December 27, 2001, 16:55:40 ; Search time 45.66 seconds
(without alignments)
749.622 Million cell updates/sec

Title: US-09-830-647-2
Perfect score: 1206
Sequence: 1 MNSGAMRIHSKGHFQGGIQV...........LKKFVKVEDMSQSPAVHLM 234

Scoring table:
Scoring table: Gapop 10.0 , Gapext 0.5
BLOSUM62
Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	1206	100.0	234	4	Q9Y2M6	q9y2m6 homo sapien
2	1170	97.0	674	2	Q90BU7	homo sapien
3	1077	89.3	676	2	Q99MU0	cricetulus
4	974	80.8	321	11	Q9CXF2	mus musculu
5	974	80.8	663	11	Q9QZ41	mus musculu
6	784	65.0	601	4	O75226	homo sapien
7	208	17.2	170	4	Q9H912	homo sapien
8	170	14.1	1695	5	Q9U9R5	drosophila
9	170.5	14.1	1695	5	Q9NK53	drosophila
10	170.5	14.1	1711	5	Q9VJL0	drosophila
11	170.5	14.1	1711	5	Q9U9R4	drosophila
12	114.5	9.5	647	3	Q93843	emericella
13	101.5	8.4	779	10	081287	arabidopsis
14	101	8.4	957	2	Q9AHL1	borrelia bu
15	99	8.2	849	2	Q9AHK4	borrelia bu
16	98	8.1	1173	2	Q9AHK6	borrelia bu
17	97	8.0	667	5	Q9Y117	drosophila
18	97	8.0	917	6	Q9TUB5	sus scrofa
19	95	7.9	1065	2	Q9AHK8	borrelia bu
20	94.5	7.8	667	2	Q9KK28	streptococc
21	94.5	7.8	1438	2	Q90KK8	staphylococ
22	92	7.6	1065	2	Q9AHK9	borrelia bu
23	91.5	7.6	681	2	Q9KK13	streptococc
24	90	7.5	219	2	Q92LV6	helicobacte
25	90	7.5	616	13	Q9W721	brachydanio
26	89.5	7.5	1065	2	Q9AHK7	borrelia bu
27	89	7.4	509	5	O15712	parmecium
28	89	7.4	528	5	O15712	parmecium
29	89	7.4	710	2	Q9VQN2	drosophila
30	89	7.4	871	8	Q35064	marchantia
31	89	7.4	1119	2	Q91YE6	arabidopsis
32	88.5	7.4	2091	5	O51228	borrelia bu
33	88.5	7.4	657	2	Q9VJ69	drosophila
34	88	7.3	680	2	Q9KK29	streptococc
35	88	7.3	805	4	Q9KK11	streptococc
36	87.5	7.3	392	2	Q95692	homo sapien
37	87.5	7.3	506	5	O50873	caenorhabdi
38	87.5	7.3	520	2	O84054	chlamydia t
39	87.5	7.3	715	10	O18822	caenorhabdi
40	87	7.2	426	2	Q91NL9	arabidopsis
41	87	7.2	1503	5	Q9KU5	vibrio chol
42	86.5	7.2	590	5	Q9V6P4	drosophila
43	86.5	7.2	869	2	O18413	caenorhabdi
44	86.5	7.2	887	11	O88763	rattus norv
45	86.5	7.2	1274	5	O60985	dictyosteli

ALIGNMENTS

RESULT 1

Q9Y2M6

```
ID   Q9Y2M6      PRELIMINARY;   PRT;   234 AA.
AC   Q9Y2M6;
DT   01-NOV-1999 (TREMBLrel. 12, Created)
DT   01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE   ACTIVATOR OF S PHASE KINASE.
GN   ASK/ H37.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kumagai H., Sato N., Yamada M., Mahony D., Seghezzi W., Lees E.,
RA   Arai K., Masai H.;
RT   "A Novel Growth- and Cell Cycle-Regulated Protein, ASK, Activates
RT   Human Cdc7-Related Kinase and Is Essential for G1/S transition in
RT   Mammalian Cells.";
RL   Mol. Cell. Biol. 0:0-0(1999).
DR   EMBL; AB028070; BAA78327.1; -.
DR   InterPro; IPR001357; BRCT.
DR   SMART; SM00292; BRCT; 1.
SQ   SEQUENCE   234 AA;   26124 MW;   50357B9FCFB472BC CRC64;
```

Query Match   100.0%;   Score 1206;   DB 4;   Length 234;
Best Local Similarity   100.0%;
Matches   234;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy   1  MNSGAMRIHSKGHFQGGIQVKNEKNRPSLKSLKTDNRPEKSKGCKPLWGKVFYLDLPSVTI 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  MNSGAMRIHSKGHFQGGIQVKNEKNRPSLKSLKTDNRPEKSKGCKPLWGKVFYLDLPSVTI 60

Qy  61  SEKLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  SEKLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 120

Qy 121  PSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYIE 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121  PSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYIE 180
```

```
Qy      181  QKKELYLLKKSSTSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQSPAVHLM 234
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  QKKELYLLKKSSTSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQSPAVHLM 234


RESULT  2
Qy  Q9UBU7
ID      Q9UBU7              PRELIMINARY;     PRT;    674 AA.
AC      Q9UBU7;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE      ACTIVATOR OF S PHASE KINASE.
GN      ASK/H37 OR DBF4.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kumagai H., Sato H., Yamada M., Mahony D., Seghezzi W., Lees E.,
RA      Arai K., Masai H.;
RT      "A Novel Growth- and Cell Cycle-Regulated Protein, ASK, Activates
RT      Human Cdc7-Related Kinase and is Essential for G1/S transition in
RT      Mammalian Cells.";
RL      Mol. Cell. Biol. 0:0-0(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Jiang W., Hunter T.;
RT      "Mammalian Cdc7/Dbf4 Protein Kinase Complex is Essential for
RT      Initiation of DNA Replication.";
RL      Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Hollingsworth R.;
RT      "Use of a semi-automated yeast two-hybrid system to identify proteins
RT      that interact with the human Cdc7 protein.";
RL      Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AB026069; BAA78326.1; -.
DR      EMBL; AF162049; AAD41911.1; -.
DR      EMBL; AF160876; AAD45357.1; -.
DR      InterPro; IPR001357; BRCT.
DR      SMART; SM00292; BRCT; 1.
SQ      SEQUENCE 674 AA;  76857 MW;  353FE87E85507E5C CRC64;

Query Match             97.0%;  Score 1170;  DB 4;  Length 674;
Best Local Similarity  100.0%;  Pred. No. 2.7e-88;
Matches  227;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1    MNSGAMRIHSKGHFQQGGIQVKNEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTI 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1    MNSGAMRIHSKGHFQQGGIQVKNEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTI 60

Qy      61   SEKLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61   SEKLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 120

Qy      121  PSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYYIE 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  PSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYYIE 180

Qy      181  QKKELYLLKKSSTSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQ 227
             ||||||||||||||||||||||||||||||||||||||||||||||
Db      181  QKKELYLLKKSSTSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQ 227


RESULT  3
Qy  Q99MU0
ID      Q99MU0              PRELIMINARY;     PRT;    676 AA.
AC      Q99MU0;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE      DBF4/ASK.
OS      Cricetulus griseus (Chinese hamster).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC      Cricetulus.
OX      NCBI_TaxID=10029;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Guo B., Lee H.;
RX      MEDLINE=21147935; PubMed=11250080;
RT      "Cloning and characterization of Chinese hamster homologue of yeast
RT      DBF4 (chDBF4).";
RL      Gene 264:249-256(2001).
DR      EMBL; AF292400; AAK21856.1; -.
SQ      SEQUENCE 676 AA;  75849 MW;  EC7EEBD80D4O38C CRC64;

Query Match             89.3%;  Score 1077;  DB 11;  Length 676;
Best Local Similarity   89.9%;  Pred. No. 1.3e-80;
Matches  205;  Conservative  13;  Mismatches  10;  Indels  0;  Gaps  0;

Qy      1    MNSGAMRIHSKGHFQQGGIQVKNEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTI 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1    MNSGAMRIHSKGHFQQGGIQVKNEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTI 60

Qy      61   SEKLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 120
             ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db      61   SEKLQKDIKDLGGRVEEFLSKDISYLVSNKKEAKFAQTLGVSPVPSPESAYTAETTSPH 120

Qy      121  PSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYYIE 180
             |||||||||||||:|||:|||||||:||||||||||||||||||:||||||||||||||||
Db      121  PSHDGSSFKSPDRVCLSRGKLLAEKAVKDHDFIPANSILSNALTWGVKILHIDDIRYYIE 180

Qy      181  QKKELYLLKKSSTSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQS 228
             |||||||:| |||||||||||:||||:|||||||||||||:||||:||
Db      181  QKKELCSLKKSSTSVRDGGKKAGTTIQKARTGRLKKPFLKVEDVNRS 228


RESULT  4
Qy  Q9CXF2
ID      Q9CXF2              PRELIMINARY;     PRT;    321 AA.
AC      Q9CXF2;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
```

```
RA  Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA  Hayashizaki Y.;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690(2001).
DR  EMBL; AK014480; BAB29383.1; -.
SQ  SEQUENCE 321 AA; 36324 MW; 741B172CF52A4579 CRC64;

Query Match             80.8%;  Score 974;  DB 11;  Length 321;
Best Local Similarity   82.4%;  Pred. No. 1.5e-72;
Matches  187; Conservative  15; Mismatches  25; Indels  0; Gaps  0;

Qy    1 MNSGAMRIHSKGHFQGGIGQVKNEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTI 60
          ||  ||||||||| ||||||| ||||||||||||||| ||| | |||||||||||||| :||
Db    1 MNLETMRIHSKAPLPGGIGQDRNEKNRPSLKSLKADNRLEKSKYRPLWGKIFYLDLPSITI 60

Qy   61 SEKLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 120
          :|||||||  ||||||||||||||  |||||||| ||||||  :|||||||||||||||||
Db   61 CEKLQKDIKELGGRVEEFLSKDISYFVSNKKEAKYAQTLGRVSPVPSPESAYTAETTSPH 120

Qy  121 PSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYYIE 180
          ||||||||||| :|||||||||| ||| :|||||||:||||||||||||||||||||||||
Db  121 PSHDGSSFKSQDRVCLSRGKLLAEKAVKDHDFIPANSILSNALSWGVKILHIDDIRYYIE 180

Qy  181 QKKKELYLLKKSSTSVSRDGGKRVGSGAQKTRTGRLKKPFLKVEDVNR 227
          ||||| :|| ||:| || || |||||||||||||||||:||||:||::
Db  181 QKKKALSALKKSSASGKDAGKKAGPGIQKTRTGRLKKPFLKVEDVNR 227
```

```
RESULT 5
ID  Q9Z41         PRELIMINARY;   PRT;   663 AA.
AC  Q9Z41;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  DBF4-RELATED PROTEIN.
GN  ASK OR MUDBF4.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99444905; PubMed=10517317;
RA  Lepke M., Puetter V., Staib C., Kneissl M., Berger C., Hoehn K.,
RA  Nanda I., Schmid M., Grumnt F.;
RT  "Identification, characterization and chromosomal localization of the
RT  cognate human and murine DBF4 genes.";
RL  Mol. Gen. Genet. 262:220-229(1999).
DR  EMBL; AJ003132; CAB56847.1; -.
DR  MGD; MGI:1351328; Ask.
SQ  SEQUENCE 663 AA; 74175 MW; 72E05CB87C3B1650 CRC64;

Query Match             80.8%;  DB 11;  Length 663;
Best Local Similarity   82.4%;  Pred. No. 3.9e-72;
Matches  187; Conservative  15; Mismatches  25; Indels  0; Gaps  0;

Qy    1 MNSGAMRIHSKGHFQGGIGQVKNEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTI 60
          ||  ||||||||| ||||||| ||||||||||||||| ||| | |||||||||||||| :||
Db    1 MNLETMRIHSKAPLPGGIGQDRNEKNRPSLKSLKADNRLEKSKYRPLWGKIFYLDLPSITI 60

Qy   61 SEKLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 120
          :|||||||  ||||||||||||||  |||||||| ||||||  :|||||||||||||||||
Db   61 CEKLQKDIKELGGRVEEFLSKDISYFVSNKKEAKYAQTLGRVSPVPSPESAYTAETTSPH 120

Qy  121 PSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYYIE 180
          ||||||||||| :|||||||||| ||| :|||||||:||||||||||||||||||||||||
Db  121 PSHDGSSFKSQDRVCLSRGKLLAEKAVKDHDFIPANSILSNALSWGVKILHIDDIRYYIE 180

Qy  181 QKKKELYLLKKSSTSVSRDGGKRVGSGAQKTRTGRLKKPFLKVEDVNR 227
          ||||| :|| ||:| || || |||||||||||||||||:||||:||::
Db  181 QKKKALSALKKSSASGKDAGKKAGPGIQKTRTGRLKKPFLKVEDVNR 227
```

```
Db  181 QKKKALSALKKSSASGKDAGKKAGPGIQKTRTGRLKKPFLKVEDVNR 227
```

```
RESULT 6
ID  O75226        PRELIMINARY;   PRT;   601 AA.
AC  O75226;
DT  01-NOV-1998 (TrEMBLrel. 08, Created)
DT  01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT  01-NOV-2001 (TrEMBLrel. 08, Last annotation update)
DE  WUGSC:H_RG135C18.1 PROTEIN (FRAGMENT).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kellen J., Burkhart J.;
RT  "The sequence of Homo sapiens BAC clone RG135C18.";
RL  Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Waterston R.;
RL  Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AC005164; AAC23786.1; -.
FT  NON_TER       1       1
SQ  SEQUENCE 601 AA; 68666 MW; 7FC90B0234C1345F CRC64;

Query Match             65.0%;  Score 784;  DB 4;  Length 601;
Best Local Similarity  154;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   74 RVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 133
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    1 RVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 60

Qy  134 VCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYYIEQKKKELYLLKKSS 193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYYIEQKKKELYLLKKSS 120

Qy  194 TSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQ 227
          ||||||||||||||||||||||||||||||||||
Db  121 TSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQ 154
```

```
RESULT 7
ID  Q9H912        PRELIMINARY;   PRT;   170 AA.
AC  Q9H912;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE  CDNA FLJ13087 FIS, CLONE NT2RP3002099.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA  Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA  Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA  Takahashi M., Chiba Y., Ishida S., Murakawa K., Kondo H.,
RA  Watanabe S., Kimura K., Mirakami K., Ishii S., Kawai Y., Takiguchi S.,
RA  Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Saito K.,
RA  Ninomiya K., Iwayanagi T.;
RL  "NEDO human cDNA sequencing project.";
RL  Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AK023149; BAB14431.1; -.
SQ  SEQUENCE 170 AA; 18392 MW; C93EE702A59B282E CRC64;
```

```
Query Match             100.0%;  DB 4;  Length 601;
Best Local Similarity   154;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Matches  154;

Qy    1 MNSGAMRIHSKGHFQGGIGQVKNEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTI 60
          ||  ||||||||| ||||||| ||||||||||||||| ||| | |||||||||||||| :||
Db    1 MNLETMRIHSKAPLPGGIGQDRNEKNRPSLKSLKADNRLEKSKYRPLWGKIFYLDLPSITI 60

Qy   61 SEKLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESAYTAETTSPH 120
          :|||||||  ||||||||||||||  |||||||| ||||||  :|||||||||||||||||
Db   61 CEKLQKDIKELGGRVEEFLSKDISYFVSNKKEAKYAQTLGRVSPVPSPESAYTAETTSPH 120

Qy  121 PSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYYIE 180
          ||||||||||| :|||||||||| ||| :|||||||:||||||||||||||||||||||||
Db  121 PSHDGSSFKSQDRVCLSRGKLLAEKAVKDHDFIPANSILSNALSWGVKILHIDDIRYYIE 180

Qy  181 QKKKELYLLKKSSTSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQ 227
          |||||||||||||:|:||| ||||||||||||||||||:||||:|::
Db  121 PSHDGSSFKSQDRVCLSRGKLLAEKAVKDHDFIPANSILSNALSWGVKILHIDDIRYYIE 180
```

```
Qy   21 KNEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTISEKLQKDIKDLGGRVEEFLS 80
          | |||         |||||  |       ||  | ||   ||| ||  |  || ||||
Db   35 KCQKNSPGARK------------HPFSGKRSFYLDLPAGKNLQFLIGAIQOLGGVIEGFLS 82

Qy   81 KDISYLISNKKEAKFAQTLGRI------SPVPSPESAYTAETTSPHPSHDGSSFKSPDTVC 135
          |||  ||  | |||                |  |||     || | || || ||| |
Db   83 KEVSYIVSSRREVK-AESSGKSHRGCPSPSPSEVRVEFSAWDPKGSHPPRSRKPVDSVP 141

Qy  136 LSRGKLLVEKAIIKDHDFIPSNSILSNALSWG 166
          |||| ||   | |       ||||||| ||| |
Db  142 LSRGKELLQKAIR------------NQVSWG 160
```

RESULT 8

```
ID   Q9U9R5        PRELIMINARY;      PRT;   1695 AA.
AC   Q9U9R5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CHIFFON.
GN   CHIF OR CHIFFON OR BG:DS09218.2 OR CG5813.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON-S;
RA   Landis G.N., Tower J.;
RT   "The Drosophila chiffon gene is required for chorion gene
RT   amplification and is related to the yeast Dbf4 regulator of DNA
RT   replication and cell cycle.";
RL   Development 126.0-0(1999);
EMBL; AF158178; AAD48779.1; -.
FlyBase; FBgn0000307; chif.
InterPro; IPR000637; AT_hook.
Pfam; PF02178; AT_hook; 1.
SMART; SM00384; AT_hook; 1.
SEQUENCE  1695 AA;  188080 MW;  1409DD8A1587C4B0 CRC64;
```

```
Query Match             14.1%;  Score 170.5; DB 5;  Length 1695;
Best Local Similarity   26.8%;  Pred. No. 2.2e-05;  Matches  78; Indels  41; Gaps  9;
Matches     59;  Conservative   42;  Mismatches

Qy   27 PSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTISEKLQKDIKDLGGRVEEFLSKDISYL 86
          || |   |  ||  || |  |||  |   |||| |  |  ||| | |||| |||  |
Db   59 RPLCHFKFYLDICDHQLAKRIESDIKALGGHLEFFLSDDITHF 83

Qy   87 ISNKKEAKFAQTLGRISPVPSPESAYTAETTSPHPSHDGSSFK-----SPDTVCLSRGKL 141
          |        |||   |   ||||           |||||  |   |
Db   84 VTDKPE-----VIGGTSGTPGTPST-PGTPTSHYQQNDGSARKPNORQSRADAILSRVR 137

Qy  142 LVEKAIIKDHDFIPSNSILSNALSWGVKILHIDDIRYIEQKKKEL--YLLKKSTSVRDG 199
          |   |   |||||   | | | | |     |  |   || ||  || |
Db  138 STVGVVNSGNSTPTTSLKRSYTIW-------QTDYAQRFIKRIQTELKQYL------E 182

Qy  200 GKRVGSGAQKTRTG----RLKKPVVKVEDMSQS--PAVHLM 234
          ||     ||         |   |  | |||  |  ||
Db  183 GKKECGGGSTSASPHHIQLKKQYVIESVKRNYRPYYHLI 222
```

RESULT 9

```
ID   Q9NK53        PRELIMINARY;      PRT;   1695 AA.
AC   Q9NK53;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
```

```
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CHIF PROTEIN.
GN   CHIF OR BG:DS09218.2 OR CG5813.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Y, AND CN BW SP;
RX   MEDLINE=99403001; PubMed=10471707;
RA   Celniker S., Rubin G.M.;
RT   "An exploration of the sequence of a 2.9-Mb region of the genome of
RT   Drosophila melanogaster: the Adh region.";
RL   Genetics 153:179-219(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Y, AND CN BW SP;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
```

RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003416; AAF45011.1; -.
DR   EMBL; AE003650; AAG22437.1; -.
DR   FlyBase; FBgn0000307; chif.
DR   InterPro; IPR000637; AT_hook.
DR   InterPro; IPR001899; Gram_pos_anchor.
DR   Pfam; PF02178; AT_hook; 1.
DR   SMART; SM00384; AT_hook; 1.
DR   PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SQ   SEQUENCE 1695 AA; 188046 MW; B3E85B35C3D4FA0 CRC64;

Query Match   14.1%;   Score 170.5; DB 5; Length 1695;
Best Local Similarity   26.8%;   Pred. No. 2.2e-05;
Matches 59; Conservative 42; Mismatches 78; Indels 41; Gaps 9;

Qy   27 PSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTISEKLQKDIKDLGGRVEEFLSKDISYL 86
              |:|| |:|| |||||| ||| |||| || |||: |||:::
Db   32 PKVKVIKSK---------------RPLCHFKFYLDICDHQLAKRIESDIKALGGHLEFFLSDDITHF 83

Qy   87 ISNKKEAKFAQTLGRISPVPSPESAYTAETTSPHPSHDGSSFK------SPDTVCLSRGKL 141
              ::|| ||| | :: | :: | |||:|::
Db   84 VTDKPE-----VIGGTSGTPGTPST-PGTPTSHYQQNDGSARKPNQRQSRADAILSRVRR 137

Qy   142 LVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYIEQKKKEL--YLLKKSSTSVRDG 199
              :|:|:|||::| |::| |:|| || | | ||:||:|:
Db   138 STVGVVNSGNSTPPTSLKRSYTIW-----QTDYAQRFIKRIQTELKQYL----------E 182

Qy   200 GKRVGSGAQKTRTG---RLKKPFVKVEDMSQS--PAVHLM 234
              ||| :| | ::|| |||| |::| : ||||
Db   183 GKKEGGGGSTSASPHHIQLKKQYVKIESVKRNYRPYHLI 222

RESULT 10
ID   Q9VJL0
AC   Q9VJL0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CHIF PROTEIN.
GN   CHIF OR BG:DS09218.2 OR CG5813.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nixon K.A., Nusskern D.R., Pacleb J.M., Palazzolo M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003650; AAF53350.1; -.
DR   FlyBase; FBgn0000307; chif.
DR   InterPro; IPR000637; AT_hook.
DR   Pfam; PF02178; AT_hook; 1.
DR   SMART; SM00384; AT_hook; 1.
SQ   SEQUENCE 1711 AA; 189216 MW; 4CF179D974817BDA CRC64;

Query Match   14.1%;   Score 170.5; DB 5; Length 1711;
Best Local Similarity   26.8%;   Pred. No. 2.3e-05;
Matches 59; Conservative 42; Mismatches 78; Indels 41; Gaps 9;

Qy   27 PSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTISEKLQKDIKDLGGRVEEFLSKDISYL 86
              |:|| |:|| |||||| ||| |||| || |||: |||:::
Db   32 PKVKVIKSK---------------RPLCHFKFYLDICDHQLAKRIESDIKALGGHLEFFLSDDITHF 83

Qy   87 ISNKKEAKFAQTLGRISPVPSPESAYTAETTSPHPSHDGSSFK------SPDTVCLSRGKL 141
              ::|| ||| | :: | :: | |||:|::
Db   84 VTDKPE-----VIGGTSGTPGTPST-PGTPTSHYQQNDGSARKPNQRQSRADAILSRVRR 137

Qy   142 LVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYIEQKKKEL--YLLKKSSTSVRDG 199
              :|:|:|||::| |::| |:|| || | | ||:||:|:
Db   138 STVGVVNSGNSTPPTSLKRSYTIW-----QTDYAQRFIKRIQTELKQYL----------E 182

Qy   200 GKRVGSGAQKTRTG---RLKKPFVKVEDMSQS--PAVHLM 234
              ||| :| | ::|| |||| |::| : ||||
Db   183 GKKEGGGGSTSASPHHIQLKKQYVKIESVKRNYRPYHLI 222

RESULT 11
ID   Q9U9R4
AC   Q9U9R4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CHIFFON-2.
GN   CHIF OR CHIFFON OR BG:DS09218.2 OR CG5813.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON-S;
RA   Landis G.N., Tower J.;
RT   "The Drosophila chiffon gene is required for chorion gene
RT   amplification and is related to the yeast Dbf4 regulator of DNA
RT   replication and cell cycle.";
RL   Development 126:0-0(1999).
DR   EMBL; AF158179; AAD48780.1; -.
DR   FlyBase; FBgn0000307; chif.
DR   InterPro; IPR000637; AT_hook.
DR   Pfam; PF02178; AT_hook; 1.
DR   SMART; SM00384; AT_hook; 1.
SQ   SEQUENCE 1711 AA; PRELIMINARY; PRT; 1711 AA.

Query Match   14.1%;   Score 170.5; DB 5; Length 1711;
Best Local Similarity   26.8%;   Pred. No. 2.3e-05;
Matches 59; Conservative 42; Mismatches 78; Indels 41; Gaps 9;

Qy   27 PSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTISEKLQKDIKDLGGRVEEFLSKDISYL 86
              |:|| |:|| |||||| ||| |||| || |||: |||:::
Db   32 PKVKVIKSK---------------RPLCHFKFYLDICDHQLAKRIESDIKALGGHLEFFLSDDITHF 83

Qy   87 ISNKKEAKFAQTLGRISPVPSPESAYTAETTSPHPSHDGSSFK------SPDTVCLSRGKL 141
              ::|| ||| | :: | :: | |||:|::
Db   84 VTDKPE-----VIGGTSGTPGTPST-PGTPTSHYQQNDGSARKPNQRQSRADAILSRVRR 137

Qy   142 LVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYIEQKKKEL--YLLKKSSTSVRDG 199
              :|:|:|||::| |::| |:|| || | | ||:||:|:
Db   138 STVGVVNSGNSTPPTSLKRSYTIW-----QTDYAQRFIKRIQTELKQYL----------E 182

Qy   200 GKRVGSGAQKTRTG---RLKKPFVKVEDMSQS--PAVHLM 234
              ||| :| | ::|| |||| |::| : ||||
Db   183 GKKEGGGGSTSASPHHIQLKKQYVKIESVKRNYRPYHLI 222

```
SQ   SEQUENCE   1711 AA;  189250 MW;  B7D0F95517C4B9A9 CRC64;

Query Match
Best Local Similarity  26.8%;  Score 170.5;  DB 5;  Length 1711;
Matches  59;  Conservative  42;  Mismatches  78;  Indels  41;  Gaps  9;

Qy   27  PSLKSLKTDNRPEKSKCKPLMGKVFYLDLPSVTISEKLQKDIKDLGGRVEEFLSKDISYL  86
            :|.|.|        |  |||||.  :|.:||:||.|||||||||.||||||||:|:|:
Db   32  PKVKVIKSK-------RPLCHFKFYLDICDHQLAKRIESDIKALGGHLEFFLSDDIHF  83

Qy   87  ISNKKEAKFAQTLGRISPVPSPESAYTAETTSPHPSHDGSSFK------SPDTVCLSRGKL  141
            :||.         .|:|.:             |||||||||:||:.      .::||||.||
Db   84  VTDKPE-----VIGGTSGTPGTPST-PGTPTSHYQQNDGSARKPNQPQSRADAILSRVVR  137

Qy  142  LVEKAIKDHDFIPSNSILSNALSWGVRILHIDDIRYYIEQKKKEL--YLLKKSSTSVRDG  199
            .:|.:       :    :. :.:.     ..|  .: :::| :::|  :|: :.:
Db  138  STVGVVNSGNSTPTTSLKRSYTIW------QTDYAQRFIKRIQTELKQYL---------E  182

Qy  200  GKRVGSGAQKTRFG---RLKKPFVKVEDMSQS--PAVHLM  234
            ||:.|.|.:.:  :   .|||||:||::..:|:  |.:||:
Db  183  GKKEGGGGSTSASPHHIQLKKQYVKIESVKRNRPYYHLI  222


RESULT  12
ID   O93843          PRELIMINARY;  PRT;  647 AA.
AC   O93843;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   G1/S REGULATOR.
GN   NIMO
OS   Emericella nidulans (Aspergillus nidulans).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=5072;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R153;
RA   James S.W.; Prasauckas K.A.; Scacheri P.C., Gygax S.E., Matura R.A.,
RA   Bullock K.A.;
RT   "nimo gene of Aspergillus nidulans.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF014812; AAD01519.1; -.
SQ   SEQUENCE   647 AA;  72842 MW;  A84A547CFB3D0EF1 CRC64;

Query Match
Best Local Similarity  18.8%;  Score 114.5;  DB 3;  Length 647;
Matches  50;  Conservative  44;  Mismatches  87;  Indels  85;  Gaps  9;

Qy   14  FQGGIQVKNEKNRPSLKSLKTDNRPEKSKCKPLWGK---------VFYLDLPSVTISEKL  64
            |.:.:           .|:              |::|:         :|||||||:||||
Db  102  FEKKLVAARDKRPQKATKQEKPPAENISIRQWQRHYRKAFPHFVYFYFDAVPIDVRSKC  161

Qy   65  QKDIKDLGGRVEEFLSKDISYLISNKKEARKFAQTLGRISPVPSPESAYTAET-----TSP  119
            .::: .||.|||||:::::|.|:|.        .||.:|:|||||||||:||:|     |.|
Db  162  SRQVIALGAREEKFSRLVTHVVISR------PIP-PEIDRRAQTGHTQDTFN  207

Qy  120  HPSHDGSSFKSPD--------TVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKI  169
            .: |          .       |.|| .:      |::    :      .::.:.|.|:
Db  208  ESAGDGAMLQTVNPAELEMHLHLAVCPKRFQ-----SQDVLHRAREMGMKI  253

Qy  170  LHIDDIRYYIEQKKKELYLLKKSSTSVRDGGKRVGSGAQKTRTGR----------  214
            |.|   : :::| :::|  :|: :.:.|.||.:.|.|.:.:.   :
Db  254  WAVEKLQRMI-ATINDIDLTNGSGHSTRNN-----AAGSQTKSRGKDLSQVLQNELNGPS  308

Qy  215  ---------LKKPFVKVEDMSQ  227
                     |||||:||.||.|:
Db  309  DRSHLSVLKDLVPFKGPFIVHDMDE  334
```

```
RESULT  13
ID   O81287          PRELIMINARY;  PRT;  779 AA.
AC   O81287;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   T14P8.6 PROTEIN (AT4G02460 PROTEIN).
DE   T14P8.6 OR AT4G02460.
GN   T14P8.6 OR AT4G02460.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   WASHU;
RT   "The A. thaliana Genome Sequencing Project.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Kalicki J., Elliott G., Cloud J.;
RT   "The sequence of A. thaliana T14P8.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Waterston R.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Lamar B.; Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
RA   Mayer K.F.X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF062098; AAC19275.1; -.
DR   EMBL; AL161494; CAB80739.1; -.
DR   HSSP; P23367; 1BKN.
DR   InterPro; IPR002099; DNA_mis_repair.
DR   InterPro; IPR003594; HATPase_c.
DR   Pfam; PF01119; DNA_mis_repair; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; UNKNOWN_1.
SQ   SEQUENCE   779 AA;  86431 MW;  B86613991FFC691 CRC64;

Query Match
Best Local Similarity  22.9%;  Score 101.5;  DB 10;  Length 779;
Matches  48;  Conservative  35;  Mismatches  66;  Indels  61;  Gaps  9;

Qy   23  EKNRPSLKSLKTDNRP--EKSK------CKPLWGK------VFYLD------LPSVTISE  62
            ||:.|||         :  ||||       |||:|||      |||||      |||:||:|
Db  392  EKENPSLREVEIDNSSPMEKFKFEIKACGTKKGEGSLSVHDVTHLDKTPSKGLPQLNVTE  451

Qy   63  KLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQ--------TLGR----ISPVPSPES  110
            |::.|:.|| .|         .|::::: |    |.|        .|||    |||||||||
Db  452  KVTDASKDLSSR--------SSFAQSTLNTFVTMGKRKHENISTLSETP  493

Qy  111  AYTAETTSPHPSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPS--NSILSNALSWGVK  168
            ..||:.|:.                   |:.|:|. :.:     ||  ||:|||||||||
Db  494  VLRNQTSSYRVEKSKFEVRALASRCLVEGDQLDDMVISKEDMTPSERDSELGNRISPGTQ  553

Qy  169  ILHID--------DIRYIIEQKKKELYL  189
            |:|:|        |||||:|||||||:|
Db  554  ADNVERHERVLGQFNLGFIIAKLERDLFIV  583


RESULT  14
```

```
Q9AHL1
ID   Q9AHL1;      PRELIMINARY;   PRT;   957 AA.
AC   Q9AHL1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   LMP1.
GN   LMP1.
OS   Borrelia burgdorferi (Lyme disease spirochete).
OC   Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dunn J.J.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF305601; AAK18799.1; -.
SQ   SEQUENCE 957 AA; 109700 MW; BE362F3EDCCE7024 CRC64;

Query Match             8.4%;  Score 101;  DB 2;  Length 957;
Best Local Similarity  22.0%;
Matches   56;  Conservative  47;  Mismatches 101;  Indels  50;  Gaps  13;

Qy   22 NEKNRPSLKSLKIDNRPEKSKCKP---LWGKVF--YLDLPSVTISEKLQKDIKDLG---- 72
Db  249 NNNNTTSLKKIPSNSQKESELSPPSQTIIGKIYRPY---SYLIKKELYEILDDINTGRV 304

Qy   73 ----GRVEEFLSKDIS------------YLISNKKEAKFAQ---------------TLGRISPVPSPE 109
Db  305 TLGKNRLKELIKKGLSNKFQKVNELIENSKNKEASNLLTLIKKDIEPNLINIPKDPYKK 364

Qy  110 SAYTAETTSPHPSHDG---SSFKSPDTVCLSRGKLLVEKAIKD-HDFI---PSNSILSNA 162
Db  365 EIFQLDKEDKNPQHPGDLKSKVHSIKPIDLENTKSR-QQAIKDLNEFLKNNPNDAQASKT 423

Qy  163 LSWGVKILHIDDIRYYIEQ-KKKELYLLKKSSTSVRDGG---KRVGSGAQKTRGRLKKP 218
Db  424 LAQANKIQHLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFLKNNPNDAQASKTLAQANK 483

Qy  219 FVKVEDMSQSPAVH 232
Db  484 IQYLEDLKSK--VH 495
```

Search completed: December 27, 2001, 16:55:42
Job time: 242 sec

```
RESULT 15
Q9AHK4
ID   Q9AHK4;      PRELIMINARY;   PRT;   849 AA.
AC   Q9AHK4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   LMP1.
GN   LMP1.
OS   Borrelia burgdorferi (Lyme disease spirochete).
OC   Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dunn J.J.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF305611; AAK18803.1; -.
SQ   SEQUENCE 849 AA; 97432 MW; 095DCC4DEACD69DF CRC64;

Query Match             8.2%;  Score 99;  DB 2;  Length 849;
Best Local Similarity  22.2%;  Pred. No. 7.3;
Matches   52;  Conservative  45;  Mismatches  89;  Indels  48;  Gaps  12;

Qy   22 NEKNRPSLKSLKIDNRPEKSKCKP---LMGKVF--YLDLPSVTISEKLQKDIKDLG---- 72
Db  249 NNNNTTSLKKIPSNSQKESELSPPSQTIIGKIYRPY---SYLIKKELYEILDDINTGRV 304
```